STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/003,211A_

Source: _1FW16_

Date Processed by STIC: _4/4/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: *10/003, 211A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                         prevent "wrapping."

2____Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
      Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
                         ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                         each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
                         residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                         previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                         the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                         Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                         This sequence is intentionally skipped
                         Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
      (NEW RULES)   <210> sequence id number
                         <400> sequence id number
                         000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                         In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
       Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                         is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
                         of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
                         Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
                         explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
                         Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                         listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFW16

RAW SEQUENCE LISTING   DATE: 04/04/2006
PATENT APPLICATION: US/10/003,211A   TIME: 08:08:04

          Input Set : A:\PTO.RJ.txt
          Output Set: N:\CRF4\04042006\J003211A.raw

     3 <110> APPLICANT: Browning, Jeffrey et al.
     6 <120> TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and Anti-
Lymphotoxin Receptor and Ligand
     7   Antibodies as Therapeutic Agents for the Treatment of Immunological
Diseases
    10 <130> FILE REFERENCE: BGN-A013CN
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/003,211A
C--> 13 <141> CURRENT FILING DATE: 2001-10-31
    15 <150> PRIOR APPLICATION NUMBER: PCT/US97/19436
    16 <151> PRIOR FILING DATE: 1997-10-24
    18 <150> PRIOR APPLICATION NUMBER: 60/029,060
    19 <151> PRIOR FILING DATE: 1996-10-25
    21 <160> NUMBER OF SEQ ID NOS: 3
    23 <170> SOFTWARE: FastSEQ for Windows Version 4.0

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 197
    27 <212> TYPE: PRT
    28 <213> ORGANISM: Homo Sapien
    30 <400> SEQUENCE: 1
    31 Ser Gln Pro Gln Ala Val Pro Pro Tyr Ala Ser Glu Asn Gln Thr Cys
    32 1   5   10   15
    33 Arg Asp Gln Glu Lys Glu Tyr Tyr Glu Pro Gln His Arg Ile Cys Cys
    34   20   25   30
    35 Ser Arg Cys Pro Pro Gly Thr Tyr Val Ser Ala Lys Cys Ser Arg Ile
    36   35   40   45
    37 Arg Asp Thr Val Cys Ala Thr Cys Ala Glu Asn Ser Tyr Asn Glu His
    38   50   55   60
    39 Trp Asn Tyr Leu Thr Ile Cys Gln Leu Cys Arg Pro Cys Asp Pro Val
    40 65   70   75   80
    41 Met Gly Leu Glu Glu Ile Ala Pro Cys Thr Ser Lys Arg Lys Thr Gln
    42   85   90   95
    43 Cys Arg Cys Gln Pro Gly Met Phe Cys Ala Ala Trp Ala Leu Glu Cys
    44   100   105   110
    45 Thr His Cys Glu Leu Leu Ser Asp Cys Pro Pro Gly Thr Glu Ala Glu
    46   115   120   125
    47 Leu Lys Asp Glu Val Gly Lys Gly Asn Asn His Cys Val Pro Cys Lys
    48   130   135   140
    49 Ala Gly His Phe Gln Asn Thr Ser Ser Pro Ser Ala Arg Cys Gln Pro
    50 145   150   155   160
    51 His Thr Arg Cys Glu Asn Gln Gly Leu Val Glu Ala Ala Pro Gly Thr

52   165   170   175

RAW SEQUENCE LISTING   DATE: 04/04/2006
PATENT APPLICATION: US/10/003,211A   TIME: 08:08:04

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\04042006\J003211A.raw

```
     53 Ala Gln Ser Asp Thr Thr Cys Lys Asn Pro Leu Glu Pro Leu Pro Pro
     54             180                 185                 190
E--> 55 Glu Met Ser Gly Ther
     56             195
```

invalid amino acid designation

SEQUENCE LISTING

<110> Browning, Jeffrey et al.

<120> Soluble Lymphotoxin Beta Receptor and Anti-Lymphotoxin Receptor and Ligand Antibodies as Therapeutic Agents for the Treatment of Immunological Diseases

replace with ↓

<130> BGN-A013CN

<150> <140> 09/299,139
<151> <141> 1999-04-23

These are prior data.

```
<210> 2
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2
AACTGCAGCG GCCGCCATGC GCCTGCCC 28
```

use lower-case letters for nucleotides

same error in Sequence 3

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/04/2006
PATENT APPLICATION: **US/10/003,211A**   TIME: 08:08:05

FYI

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\04042006\J003211A.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes
spaces.

Seq#:1; Line(s) 6

7

VERIFICATION SUMMARY   DATE: 04/04/2006
PATENT APPLICATION: **US/10/003,211A**   TIME: 08:08:05

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\04042006\J003211A.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application
Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:55 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:55 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:69 M:112 C: (48) String data converted to lower case,
L:80 M:112 C: (48) String data converted to lower case,